

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/960,143

DATE: 10/10/2001

TIME: 12:51:24

Input Set : A:\RTS-0266_Seq_ASCII.txt

Output Set: N:\CRF3\10102001\I960143.raw

3 <110> APPLICANT: Brenda F. Baker
 4 Susan M. Freier
 6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 8 EXPRESSION
 8 <130> FILE REFERENCE: RTS-0266
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/960,143
 C--> 10 <141> CURRENT FILING DATE: 2001-09-24
 10 <160> NUMBER OF SEQ ID NOS: 88
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 20
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 20 <223> OTHER INFORMATION: Antisense Oligonucleotide
 22 <400> SEQUENCE: 1
 23 tccgtcatcg ctccctcaggg 20
 26 <210> SEQ ID NO: 2
 27 <211> LENGTH: 20
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 33 <223> OTHER INFORMATION: Antisense Oligonucleotide
 35 <400> SEQUENCE: 2
 36 atgcattctg cccccaagga 20
 39 <210> SEQ ID NO: 3
 40 <211> LENGTH: 1639
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Homo sapiens
 44 <220> FEATURE:
 46 <220> FEATURE:
 47 <221> NAME/KEY: CDS
 48 <222> LOCATION: (91)...(390)
 50 <400> SEQUENCE: 3
 51 acaaaactttc agagacagca gagcacacaa gtttctagga caagagccag gaagaaacca 60
 53 ccggaaggaa ccatctcact gtgtgtaaac atg act tcc aag ctg gcc gtg gct 114
 54 Met Thr Ser Lys Leu Ala Val Ala
 55 1 5
 57 ctc ttg gca gcc ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt 162
 58 Leu Leu Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val
 59 10 15 20
 61 ttg cca agg agt gct aaa gaa ctt aga tgt cag tgc ata aag aca tac 210
 62 Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr
 63 25 30 35 40
 65 tcc aaa cct ttc cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag 258
 66 Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu
 67 45 50 55
 69 agt gga cca cac tgc gcc aac aca gaa att att gta aag ctt tct gat 306
 70 Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp

ENTERED

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71          60          65          70
73 gga aga gag ctc tgt ctg gac ccc aag gaa aac tgg gtg cag agg gtt      354
74 Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val
75          75          80          85
77 gtg gag aag ttt ttg aag agg gct gag aat tca taa aaaaattcat      400
78 Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
W--> 79          90          95          100
81 tctctgtggt atccaagaat cagtgaagat gccagtgaat cttcaagcaa atctacttca      460
83 acacttcatg tattgtgtgg gtctgttgta ggggtgccag atgcaatata agattcctgg      520
85 ttaaatttga atttcagtaa acaatgaata gtttttcatt gtaccatgaa atatccagaa      580
87 catacttata tgtaaagtat tattttatttg aatctacaaa aaacaacaaa taatttttga      640
89 atataaggat tttcctagat attgcacggg agaataata aatagcaaaa ttgggccaag      700
91 ggccaagaga atatccgaac ttttaatttca ggaattgaaat gggtttgcta gaatgtgata      760
93 tttgaagcat cacataaaaa tgatgggaca ataaattttg ccataaagtc aaatttagct      820
95 ggaaatcctg gatttttttc tgttaaattct ggcaacccta gtctgctagc caggatccac      880
97 aagtccttgt tccactgtgc cttgttttct cttttatttc taagtggaaa aagtattagc      940
99 caccatctta cctcacagtg atgtgtgag gacatgtgga agcactttta gttttttcat      1000
101 cataacataa attatttttca agtgttaactt attaacctat ttattattta tgtatttatt      1060
103 taagcatcaa atatttgtgc aagaatttgg aaaaatagaa gatgaatcat tgattgaata      1120
105 gttataaaga tgttatagta aatttatttt attttagata ttaaattgatg ttttattaga      1180
107 taaatttcaa tcagggtttt tagattaaac aaacaacaaa ttgggtaccc agttaaattt      1240
109 tcatttcaga taaacaacaa ataatttttt agtataagta cattattgtt tatctgaaat      1300
111 ttttaattgaa ctaacaatcc tagtttgata ctcccagtc tgtcattgcc agctgtgttg      1360
113 gtagtgcgtg gttgaattac ggaataatga gttagaacta ttaaacacgc caaaactcca      1420
115 cagtcaatat tagtaatttc ttgctggttg aaacttgttt attatgtaca aatagattct      1480
117 tataatatta tttaaatgac tgcattttta aatacaaggc tttatatttt taactttaag      1540
119 atgtttttat gtgctctcca aatttttttt actgtttctg attgtatgga aatataaaag      1600
121 taaatatgaa acatttaaaa tataatttgt tgtcaaagt      1639
124 <210> SEQ ID NO: 4
125 <211> LENGTH: 25
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
131 <223> OTHER INFORMATION: PCR Primer
133 <400> SEQUENCE: 4
134 gaaggaacca tctcactgtg tgtaa      25
137 <210> SEQ ID NO: 5
138 <211> LENGTH: 21
139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
144 <223> OTHER INFORMATION: PCR Primer
146 <400> SEQUENCE: 5
147 aaatcaggaa ggctgccaaag a      21
150 <210> SEQ ID NO: 6
151 <211> LENGTH: 23
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:

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157 <223> OTHER INFORMATION: PCR Probe
159 <400> SEQUENCE: 6
160 catgacttcc aagctggccg tgg
163 <210> SEQ ID NO: 7
164 <211> LENGTH: 19
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
170 <223> OTHER INFORMATION: PCR Primer
172 <400> SEQUENCE: 7
173 gaaggtgaag gtcggagtc
176 <210> SEQ ID NO: 8
177 <211> LENGTH: 20
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
183 <223> OTHER INFORMATION: PCR Primer
185 <400> SEQUENCE: 8
186 gaagatggtg atgggatttc
189 <210> SEQ ID NO: 9
190 <211> LENGTH: 20
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
196 <223> OTHER INFORMATION: PCR Probe
198 <400> SEQUENCE: 9
199 caagcttccc gttctcagcc
202 <210> SEQ ID NO: 10
203 <211> LENGTH: 5187
204 <212> TYPE: DNA
205 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:
208 <221> NAME/KEY: CDS
209 <222> LOCATION: (1584)...(3385)
211 <221> NAME/KEY: intron
212 <222> LOCATION: (1648)...(2463)
213 <223> OTHER INFORMATION: Intron 1
215 <221> NAME/KEY: intron
216 <222> LOCATION: (2600)...(2870)
217 <223> OTHER INFORMATION: Intron 2
219 <221> NAME/KEY: intron
220 <222> LOCATION: (2955)...(3369)
221 <223> OTHER INFORMATION: Intron 3
223 <221> NAME/KEY: exon
224 <222> LOCATION: (3370)...(4632)
225 <223> OTHER INFORMATION: Exon 4
227 <400> SEQUENCE: 10
228 gaattcagta acccagcat tattttatcc tcaagtctta ggttggttgg agaaagataa 60
229 caaaaagaaa catgattgtg cagaaacaga caaacctttt tggaaagcat ttgaaaatgg 120

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230 cattccccct ccacagtgtg ttcacagtgt gggcaaattc actgctctgt cgtacttttct 180
231 gaaaatgaag aactgtttaca ccaagggtgaa ttattttataa attatgtact tgcccagaag 240
232 cgaacagact tttactatca taagaaccct tccttgggtgt gctctttatc tacagaatcc 300
233 aagacctttc aagaaagggtc ttggattctt ttcttcagga cactaggaca taaagccacc 360
234 tttttatgat ttgttgaaat ttctcactcc atcccttttg ctgatgatca tgggtcctca 420
235 gaggtcagac ttggtgtcct tggataaaga gcatgaagca acagtggctg aaccagagtt 480
236 ggaacccaga tgctctttcc actaagcata caactttcca ttagataaca cctccctccc 540
237 accccaacca agcagctcca gtgcaccact ttctggagca taaacatacc ttaactttac 600
238 aacttgagtgt gccttgaata ctgttccat ctggaatgtg ctgttctctt tcatcttctc 660
239 ctattgaagc cctcctattc ctcaatgcct tgctccaact gcctttggaa gattctgctc 720
240 ttatgcctcc actggaatta atgtcttagt accacttgct tattctgcta tatagtcagt 780
241 ccttacattg ctttcttctt ctgatagacc aaactcttta aggacaagta cctagtctta 840
242 tctatttcta gatcccccac attactcaga aagttactcc ataaatgttt gtggaactga 900
243 tttctatgtg aagacatgtg ccccttccact ctgttaacta gcattagaaa aacaaatctt 960
244 ttgaaaagtt gtagtatgcc cctaagagca gtaacagttc ctagaaactc tctaaaatgc 1020
245 ttagaaaaag atttatttta aattacctcc ccaataaaat gattggctgg cttatcttca 1080
246 ccatcatgat agcatctgta attaactgaa aaaaaataat tatgccatta aaagaaaatc 1140
247 atccatgatc ttgttctaac acctgccact ctagtactat atctgtcaca tgggtctatga 1200
248 taaagttatc tagaaataaa aaagcataca attgataatt caccaaattg tggagcttca 1260
249 gtatttttaa tgtatattaa aattaaatta ttttaaagat caaagaaaac tttcgtcata 1320
250 ctccgtatth gataaggaac aaataggaag tgtgatgact caggtttgcc ctgaggggat 1380
251 gggccatcag ttgcaaactg tggaatttcc tctgacataa tgaaaagatg aggggtgcata 1440
252 agttctctag taggggtgatg atataaaaag ccaccggagc actccataag gcacaaactt 1500
253 tcagagacag cagagcacac aagcttctag gacaagagcc aggaagaaac caccggaagg 1560
254 aaccattctc actgtgtgta aac atg act tcc aag ctg gcc gtg gct ctc ttg 1613
255 Met Thr Ser Lys Leu Ala Val Ala Leu Leu
256 1 5 10
258 gca gcc ttc ctg att tct gca gct ctg tgt gaa ggt aag cac atc ttt 1661
259 Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Lys His Ile Phe
260 15 20 25
262 ctg acc tac agc gtt ttc cta tgt cta aat gtg atc ctt aga tag caa 1709
263 Leu Thr Tyr Ser Val Phe Leu Cys Leu Asn Val Ile Leu Arg * Gln
264 30 35 40
266 agc tat tct tga tgc ttt ggt aac aaa cat cct ttt tat tca gaa aca 1757
267 Ser Tyr Ser * Cys Phe Gly Asn Lys His Pro Phe Tyr Ser Glu Thr
268 45 50 55
270 gaa tat aat ctt agc agt caa tta atg tta aat tga aga ttt aga aaa 1805
271 Glu Tyr Asn Leu Ser Ser Gln Leu Met Leu Asn * Arg Phe Arg Lys
272 60 65 70
274 aac tat ata taa cac tta gga aat ata aag gtt tga tca ata tag ata 1853
275 Asn Tyr Ile * His Leu Gly Asn Ile Lys Val * Ser Ile * Ile
276 75 80
278 ttc tgc ttt tat aat tta tac cag gta gca tgc ata tat tta acg taa 1901
279 Phe Cys Phe Tyr Asn Leu Tyr Gln Val Ala Cys Ile Tyr Leu Thr *
280 85 90 95
282 ata agt aat tta tag tat gtc cta ttg aga acc acg gtt acc tat att 1949
283 Ile Ser Asn Leu * Tyr Val Leu Leu Arg Thr Thr Val Thr Tyr Ile
284 100 105 110
286 atg tat taa tat tga gtt gag caa ggt aac tca gac aat tcc act cct 1997

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287 Met Tyr * Tyr * Val Glu Gln Gly Asn Ser Asp Asn Ser Thr Pro
288 115 120 125
290 tgt agt att tca ttg aca agc ctc aga ttt gtc att aat tcc tgt ctg 2045
291 Cys Ser Ile Ser Leu Thr Ser Leu Arg Phe Val Ile Asn Ser Cys Leu
292 130 135 140
294 gtt taa aga tac cct gat tat aga cca ggc atg tat aac tta ttt ata 2093
295 Val * Arg Tyr Pro Asp Tyr Arg Pro Gly Met Tyr Asn Leu Phe Ile
296 145 150 155
298 tat ttc tgt taa ttc ttt ctg aag gca att tct atg ctg gag agt ctt 2141
299 Tyr Phe Cys * Phe Phe Leu Lys Ala Ile Ser Met Leu Glu Ser Leu
300 160 165 170
302 agc ttg cct act ata aat aac act gtg gta tca cag agg att atg caa 2189
303 Ser Leu Pro Thr Ile Asn Asn Thr Val Val Ser Gln Arg Ile Met Gln
304 175 180 185 190
306 tat tga cca gat aaa aat acc atg aag atg ttg ata ttg tac aaa aag 2237
307 Tyr * Pro Asp Lys Asn Thr Met Lys Met Leu Ile Leu Tyr Lys Lys
308 195 200 205
310 aac tct aac tct tat ata gga agt tgt tca atg ttg tca gtt atg act 2285
311 Asn Ser Asn Ser Tyr Ile Gly Ser Cys Ser Met Leu Ser Val Met Thr
312 210 215 220
314 gtt ttt taa aac aaa gaa cta act gag gtc aag ggc tag gag ata ttc 2333
315 Val Phe * Asn Lys Glu Leu Thr Glu Val Lys Gly * Glu Ile Phe
316 225 230 235
318 agg aat gag ttc act aga aac atg atg cct tcc ata gtc tcc aaa taa 2381
319 Arg Asn Glu Phe Thr Arg Asn Met Met Pro Ser Ile Val Ser Lys *
320 240 245 250
322 tca tat tgg aat tag aag gaa gta gct ggc aga gct gtg cct gtt gat 2429
323 Ser Tyr Trp Asn * Lys Glu Val Ala Gly Arg Ala Val Pro Val Asp
324 255 260 265
326 aaa atc aat cct taa tca ctt ttt ccc cca aca ggt gca gtt ttg cca 2477
327 Lys Ile Asn Pro * Ser Leu Phe Pro Pro Thr Gly Ala Val Leu Pro
328 270 275 280
330 agg agt gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa 2525
331 Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys
332 285 290 295
334 cct ttc cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga 2573
335 Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly
336 300 305 310
338 cca cac tgc gcc aac aca gaa att atg taa gta ctt taa aaa aga tta 2621
339 Pro His Cys Ala Asn Thr Glu Ile Met * Val Leu * Lys Arg Leu
340 315 320 325
342 gat att ttg ttt tag caa act taa aat taa gga agg tgg aaa tat tta 2669
343 Asp Ile Leu Phe * Gln Thr * Asn * Gly Arg Trp Lys Tyr Leu
344 330 335
346 gga aag ttc cag gtg tta gga tta cag tag taa atg aaa caa aac aaa 2717
347 Gly Lys Phe Gln Val Leu Gly Leu Gln * * Met Lys Gln Asn Lys
348 340 345 350
350 ata aaa ata ttt gtc tac atg aca ttt aaa tat ggt agc ttc cac aac 2765
351 Ile Lys Ile Phe Val Tyr Met Thr Phe Lys Tyr Gly Ser Phe His Asn

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3